

## Microbial indicators, pathogens and methods for their monitoring in water environment

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### ABSTRACT

Water is critical for life, but many people do not have access to clean and safe drinking water and die because of waterborne diseases. The analysis of drinking water for the presence of indicator microorganisms is key to determining microbiological quality and public health safety. However, drinking water-related illness outbreaks are still occurring worldwide. Moreover, different indicator microorganisms are being used in different countries as a tool for the microbiological examination of drinking water. Therefore, it becomes very important to understand the potentials and limitations of indicator microorganisms before implementing the guidelines and regulations designed by various regulatory agencies. This review provides updated information on traditional and alternative indicator microorganisms with merits and demerits in view of their role in managing the waterborne health risks as well as conventional and molecular methods proposed for monitoring of indicator and pathogenic microorganisms in the water environment. Further, the World Health Organization (WHO) water safety plan is emphasized in order to develop the better approaches designed to meet the requirements of safe drinking water supply for all mankind, which is one of the major challenges of the 21st century.

**Key words** | drinking water quality, fecal contamination, microbial indicator, molecular techniques, waterborne disease, water safety plan

### INTRODUCTION

Ensuring the safety of drinking water (DW) is an ongoing process. Water that looks suitable for drinking may be contaminated with pathogens that may cause serious health hazards. The microbiological examination of DW for the presence of indicator microorganisms (IMs) is key to determining microbiological quality and ensuring public health safety. The presence of IMs represents the fecal contamination of DW with pathogens and quality deterioration. The microbiological assessment of DW quality is based on the relationship between IMs and pathogens (Borrego *et al.* 2002a, 2002b; Koster *et al.* 2003; WHO 2008). However, DW illness outbreaks have occurred both in the presence and absence of IMs. This is because of either failure of treatment processes that do not completely eliminate the pathogens from DW or entry of contaminated water harboring pathogens into distribution systems through cracks/

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leakage (Figueras & Borrego 2010). In spite of specific legislation, DW illness outbreaks are still occurring worldwide and the associated control measures are being carried out (Figueras & Borrego 2010).

The World Health Organization (WHO) has published several guidelines in collaboration with the International Water Association (IWA) and the Organisation for Economic Co-operation and Development (OECD) for improvement in DW quality (Dufour *et al.* 2003; EIWID 2003; WHO 2008). Water safety plans (WSPs) are the most recent document to create awareness among water quality professionals, so that they can develop the preventive strategies to protect public health (Bartram *et al.* 2009).

Many waterborne pathogens are still difficult to detect and/or quantify due to the lack of easy and reliable methods. The specific methods that are used to detect IMs have also

been reviewed in many studies (Koster *et al.* 2003; NRC 2004). Nowadays, new approaches based on the virulence factor-activity relationship (VF-AR) to detect emerging waterborne pathogens are being explored (Karanis *et al.* 2007; Cangelosi 2009). However, the routine application of these methods for the examination of pathogens is not yet the reality and is restricted to research studies or to cases of suspected outbreaks. This review article emphasizes the traditional and alternative IMs with merits and demerits in view of their role in managing waterborne health risks, as well as conventional and molecular methods proposed for monitoring of indicator and pathogenic microorganisms in water environments. In addition, the pathogens removal efficiency of DW and wastewater treatment plants (WWTPs) is discussed. Further, WSPs are given in order to develop better approaches to meet the requirement of safe DW supply for all mankind.

The presence of indicator organisms will likely continue to be used as a criterion of DW quality and it will be useful if attention is given for the development and use of optimal methods for their recovery. The existing data also indicate that there is limited utility of IMs under certain circumstances, although there is no ideal IM and research is ongoing to search for a suitable microorganism that can indicate the presence of pathogenic microorganisms more accurately than traditional indicators.

## DRINKING WATER AS A SOURCE OF DISEASES

Water is the essence of life. A clean and safe DW supply may be the norm in European and North American countries, but in developing countries the assessment of both clean and safe DW is not the rule and hence waterborne illness outbreaks are common. In Asian and African countries, children under 5 years of age are primarily affected by diarrheal diseases (DDs) transmitted through contaminated DW (Seas *et al.* 2009). It is also reported that around two and a half billion people have no access to clean and safe DW and more than 1.5 million children die each year from DDs (Fenwick 2006). This is due to the contamination of DW with different types of pathogenic microorganisms present in urban sewage, and feces of infected humans and animals (Table 1). These include enteric bacteria, viruses and

**Table 1** | Pathogens transmitted through contaminated DW and diseases caused by them

Pathogens	Diseases
<b>Bacteria</b>	
<i>Campylobacter jejuni</i>	Gastroenteritis
Enteropathogenic <i>E. coli</i>	Gastroenteritis
<i>Legionella pneumophila</i>	Acute respiratory illness
<i>Salmonella</i>	Typhoid, paratyphoid, salmonellosis
<i>Shigella</i>	Bacillary dysentery
<i>Vibrio cholerae</i>	Cholera
<i>Yersinia enterocolitica</i>	Gastroenteritis
<b>Protozoa</b>	
<i>Cryptosporidium</i>	Diarrhea
<i>Entamoeba histolytica</i>	Amoebic dysentery
<i>Giardia lamblia</i>	Diarrhea
<i>Naegleria fowleri</i>	Meningoencephalitis
<b>Enteroviruses</b>	
<i>Adenoviruses</i>	Respiratory illness, eye infection, gastroenteritis
<i>Astroviruses</i>	Gastroenteritis
<i>Caliciviruses</i>	Gastroenteritis
<i>Coxsackievirus A</i>	Meningitis, respiratory illness
<i>Coxsackievirus B</i>	Myocarditis, meningitis, respiratory illness
<i>Echovirus</i>	Meningitis, diarrhea, fever, respiratory illness
<i>Hepatitis A viruses</i>	Infectious hepatitis
<i>Norwalk viruses</i>	Diarrhea, vomiting, fever
<i>Polioviruses</i>	Meningitis, paralysis
<i>Rotaviruses</i>	Diarrhea, vomiting

Adapted from Metcalf & Eddy (1991), AWWA (1999), Ashbolt (2004), Gerba & Smith (2005), and Arnone & Walling (2007).

parasites, and can be transmitted through contaminated water and food (NRC 2004; Toranzos *et al.* 2007; WHO 2008).

In general, any practice that involves the distribution of domestic wastewater in soil has the potential to cause microbial contamination of ground water. The wastewater discharged in fresh water and coastal seawaters is also a major source of pathogenic microbes (Fenwick 2006; WHO 2008). The wastewater treatment processes applied at WWTPs do not completely eliminate or inactivate the pathogenic microbes present in wastewater. The pathogen

**Table 2** | Pathogen removal in treated sewage

Infective dose of pathogen	Enteric viruses	Salmonella	Giardia
No. of cells or particles	1 > 10	>10 <sup>5</sup>	25–100
Amount in feces	10 <sup>6</sup> –10 <sup>10</sup> /g	10 <sup>10</sup> /g	9 × 10 <sup>6</sup> /g of stool
Concentration in raw sewage (No./L)	10 <sup>3</sup>	5,000–80,000	9,000–200,000
% Removal of pathogens during			
Primary treatment	50–98.3	95.8–99.8	27–64
Number remaining	1,700–50,000	160–3,360	72,000–146,000
Secondary treatment	53–99.92	98.65–99.996	45–96.7
Number remaining	85–47,500	3–1,075	6,480–109,500
Tertiary treatment	83–99.9999998	99.99–99.9999995	98.5–99.99995
Number remaining	0.0002–17	0.000004–7	0.099–2,951

Adapted from Yates (1998) and Toze (2006).

removal efficiency of wastewater treatment processes, as well as the concentration of pathogenic microbes that remained in digested sludge even after treatment processes, is summarized in Tables 2 and 3, respectively.

## INDICATORS OF MICROBIAL CONTAMINATION OF DRINKING WATER

The presence of enteric pathogens in DW is of great concern (Maal-Bared *et al.* 2008). Thus, the legislation in

**Table 3** | Concentration of microorganisms in digested sludge

Organisms	Type of stabilization (no./g of dry weight)	
	Anaerobic	Aerobic
<i>Enteroviruses</i>	0.2–210	0–260
<i>Rotaviruses</i>	14–485	ND
<i>Salmonella</i>	3–10 <sup>3</sup>	3
Total coliforms	10 <sup>2</sup> –10 <sup>6</sup>	10 <sup>5</sup> –10 <sup>6</sup>
Fecal coliforms	10 <sup>2</sup> –10 <sup>6</sup>	10 <sup>5</sup> –10 <sup>5</sup>
<i>Shigella</i> sp.	20	ND
<i>Yersinia enterocolitica</i>	10	ND
<i>Giardia</i> spp.	10 <sup>2</sup> –10 <sup>3</sup>	ND
<i>Ascaris</i>	–	–
<i>Trichuris</i>	–	–
<i>Toxocara</i>	–	–

Adapted from Straub *et al.* (1993) and Lepeuple *et al.* (2004).  
Average of all types of digested sludge (% viable); ND: no data.

Europe, the USA and other countries requires adequate examination of IMs to determine microbiological quality. Hence, the most useful tool to detect pathogens in the water environment is the simultaneous analysis of several microorganisms classed as ‘Indicator’ microorganisms (Ashbolt *et al.* 2001). These IMs are being used to assess the microbiological quality of environmental water (Ashbolt *et al.* 2001). However, the criterion for an ideal IM to indicate the presence of pathogens in water environments has been discussed in many studies (Tyagi *et al.* 2006; Savichtcheva & Okabe 2006; Cabral 2010; Zheng *et al.* 2013). Generally, IMs are not themselves human pathogens (Verhille 2013); this has been the foundation upon which the protection of public health from water-borne diseases (WBDs) has been developed. To avoid ambiguity in the term ‘Microbial Indicator’ the following three groups are now recognized (Table 4). The most widely used IMs are coliforms (total coliforms (TCs)), fecal or thermotolerant coliforms, *Escherichia coli*, enterococci (fecal streptococci or intestinal enterococci) and bacteriophages.

### Potential applications of an IM

The microorganism used as an indicator should also be chosen on the basis of the particular application of the information. Thus, the potential application of an IM should be to indicate:

(a) the fecal pollution;

**Table 4** | Definitions for indicator and index microorganisms of public health concern

Group	Definition
Process indicator	A group of organisms that demonstrates the efficacy of a process such as total heterotrophic bacteria or total coliforms for chlorine disinfection
Fecal indicator	A group of organisms that indicates the presence of contamination such as the bacterial groups, thermotolerant coliforms or <i>E. coli</i> . Hence, they only infer that pathogens may be present
Index and model organisms	A group/or species indicative of pathogen presence and behavior, respectively, such as <i>E. coli</i> as an index for Salmonella and F-RNA coliphages as models of human enteric viruses

Adapted from Ashbolt et al. (2001).

- (b) the presence of domestic sewage;
- (c) the presence of pathogenic microbes;
- (d) the efficiency of a particular water or wastewater treatment process;
- (e) the environmental fate of a target pathogen;
- (f) the movement of particles suspended in water during subsurface transport.

### Traditional indicators

The microorganisms that have been reported as an indicator of fecal contamination are summarized in Table 5, whereas the IMs that have been used to establish the performance criteria for various water uses are listed in Table 6.

### Coliforms or total coliforms

The coliforms belong to the family *Enterobacteriaceae*, which includes harmless *E. coli* and *Enterobacter*, the common intestinal organisms and occasional pathogens like *Klebsiella*, *Citrobacter*, *Kluyvera* and *Leclercia* genera and some members of the genus *Serratia* (Figueras & Borrego 2010). These bacteria are classically used as an indicator of fecal contamination in water because they are considered as the residents of intestinal tracts of homeothermic animals (Figueras et al. 2000; Staradumskyte & Paulauskas 2012) and, thus, are of sanitary significance. The TCs in a distribution system may provide an enhanced knowledge of water quality throughout the system as well as overall system condition. In a distribution system, the coliform bacteria act as operational indicators. Their presence indicates the deterioration in water quality, possibly via bacterial re-growth problems or post-treatment

contamination in DW that can be investigated further. The TCs are bacteria that are predominant in the natural environment. There are some limitations in the general use of coliforms as IMs, which include: (a) their ability to grow in natural water; and (b) lack of correlation between the number of coliforms and those of microbial pathogens. Furthermore, several studies have demonstrated the presence of coliforms in drinking water distribution systems (DWDS) associated with biofilm growth problems (WHO 2004; O'Reilly et al. 2007). Therefore, these can serve as an indicator of treatment efficiency of WWTPs because of their sensitivity to chlorine. However, some members of the TC group are no longer used as an indicator of fecal contamination because advances in the science of taxonomy have shown that they are not specific to the human intestine. Hence, these can also be found in the natural environment (Leclerc et al. 2001; Tallon et al. 2005; Verhille 2013). Thus, the presence of TC bacteria is not a definitive proof that the environment has been contaminated with fecal material.

### Fecal coliforms or 'thermotolerant coliforms'

Coliforms that are able to grow and ferment lactose with the production of acid and gas at 44.5 °C in the presence of bile salts are grouped as fecal coliforms (FCs) (Payment et al. 2003; WHO 2008; Staradumskyte & Paulauskas 2012). For this reason, 'thermotolerant coliforms' would be the scientifically more accurate term for this group (Fong et al. 2007; Figueras et al. 2008). Thus, the bacteria of this coliform subgroup have been found to have a positive correlation with fecal contamination of warm-blooded animals (Fenwick 2006; Fong et al. 2007; Toranzos et al. 2007). The physiological basis of the elevated temperature phenotype in FCs has

**Table 5** | Definitions of key fecal IMs

Indicator organisms	Characteristics/features
Total coliforms	Gram-negative, non-spore-forming, oxidase/indole-negative, rod-shaped facultative anaerobic bacteria that ferment lactose (with $\beta$ -galactosidase) to acid and gas within 24–48 h at $36 \pm 2$ °C in a medium containing bile salts and detergents. Not specific indicators of fecal pollution
Fecal coliforms	Thermotolerant coliforms that produce acid and gas from lactose fermentation at $44.5 \pm 0.2$ °C within $24 \pm 2$ h, also known as fecal coliforms due to their role as fecal indicators
<i>Escherichia coli</i> ( <i>E. coli</i> )	Thermophilic coliforms that produce indole from tryptophan, but also defined now as coliforms able to produce $\beta$ -glucuronidase (although taxonomically up to 10% of environmental <i>E. coli</i> may not). Most appropriate group of coliforms to indicate fecal pollution from warm-blooded animals
Fecal streptococci (FS)	Gram-positive, catalase-negative non-spore-forming cocci from selective media (e.g., azide dextrose broth (sodium azide = strong inhibitor of respiratory chain) or m-Enterococcus agar) that grow on bile aesculin agar and at 45 °C, belonging to the genera <i>Enterococcus</i> and <i>Streptococcus</i> possessing the Lancefield group D antigen. This group had been used in conjunction with fecal coliform to determine the source of recent fecal contamination (man or animals). Several strains appear to be ubiquitous and cannot be distinguished from the true fecal streptococci under usual analytical procedure, which detracts from their use as an indicator organism
Bacteroides	An anaerobic, non-spore-forming, Gram-negative, pleiomorphic bacillus, has been proposed as human-specific indicator
Enterococci	The subset of fecal streptococci that grow at pH 9.6, 10 and 45 °C and in 6.5% NaCl. Nearly all are members of the genus <i>Enterococcus</i> , and also fulfill the following criteria: resistance to 60 °C for 30 min and ability to reduce 0.1% methylene blue. Alternatively, enterococci can be directly identified as microorganisms capable of aerobic growth at $44 \pm 0.5$ °C and of hydrolyzing 4-methylumbelliferyl- $\beta$ -D-glucoside (MUD, detecting $\beta$ -glucosidase activity by blue fluorescence at 366 nm), in the presence of thallium acetate, nalidixic acid and 2, 3, 5-triphenyltetrazolium chloride (TTC, which is reduced to red formazan) in the specified medium (ISO/FDIS 7899-1 1998). The enterococci are generally found in lower numbers than other indicator organisms; however, they exhibit better survival in sea water
<i>Clostridium perfringens</i>	Gram-positive spore-forming, non-motile, strict anaerobe, sulfite-reducing bacilli, ferment lactose, sucrose and inositol with the production of gas, produce stormy clot fermentation with milk, reduce nitrate, hydrolyze gelatin and produce lecithinase and acid phosphatase. Spores most often of fecal origin and always present in sewage. These indicate the presence of Protozoa and Enteroviruses. Not all sulphite-reducing clostridia (SRC) in receiving waters are indicators of fecal pollution, hence <i>C. perfringens</i> is the appropriate indicator
Bifidobacteria	Gram-positive, obligate anaerobic, non-acid-fast, non-spore-forming, non-motile bacilli which are highly pleomorphic and may exhibit branching bulbs (bifids), clubs, coccoid, coryneform, Y and V forms. They are all catalase-negative and ferment lactose (except the three insect species; <i>B. asteroides</i> , <i>B. indicum</i> and <i>B. coryneforme</i> ) and one of the most numerous groups of bacteria in the feces of warm-blooded animals
Bacteriophages (phages)	Bacterial viruses which are ubiquitous in the environment and resistant to disinfection. For water quality testing and to model human enteric viruses and protozoans, most interest in somatic coliphages, male-specific RNA coliphages (F-RNA coliphages) and phages infecting <i>B. fragilis</i>

Adapted from Ashbolt et al. (2001).

been described as ‘thermotolerant adaptation of proteins’. Therefore, their stability at temperatures found in the enteric tracts of animals is both constant and higher than the temperature in most aquatic and terrestrial environments (Clark 1990).

However, some thermotolerant coliform bacteria that conform to this definition also belong to the genus *Klebsiella* and have been isolated from environmental samples in the apparent absence of fecal contamination (Fenwick

2006; Toranzos et al. 2007; Figueras et al. 2008). Similarly, other members of the thermotolerant coliform group including *E. coli* have been detected in some pristine areas (Hazen & Toranzos 1990). These were also associated with the re-growth events in DWDS (O’Reilly et al. 2007; Collado et al. 2010). However, the potential for re-growth or multiplication is less than that of the TCs. Therefore, caution needs to be exercised when deciding whether the presence of IMs does indeed represent fecal contamination and thus is a

**Table 6** | Indicator organisms used to establish the performance criteria for various water uses

Water use	Indicator organisms
Drinking water	Total coliforms
Freshwater recreation	Fecal coliforms ( <i>E. coli</i> )
Salt water recreation	Fecal coliforms, total coliforms and Enterococci
Shellfish-growing areas	Total coliforms, fecal coliforms
Agricultural irrigation (for reclaimed water)	Total coliforms
Wastewater effluent	Fecal coliforms
Disinfection	MS2 coliphages

Adapted from Metcalf & Eddy (2003).

threat to public health. The FCs also display a survival pattern similar to those of bacterial pathogens (Figueras *et al.* 2008). However, their usefulness as an indicator of protozoans and viral contamination is limited and hence tends to be replaced by *E. coli* in several legislations (WHO 2004).

*Escherichia coli* (mostly non-pathogenic) is the most reliable indicator of enteric pathogens. It is therefore the indicator of choice to indicate the occurrence of recent fecal contamination in DW (Leclerc *et al.* 2001; Payment *et al.* 2003; Wade *et al.* 2003; Tallon *et al.* 2005; Verhille 2013). However, only some strains of *E. coli* are capable of causing disease (Tallon *et al.* 2005; Scheutz & Strockbine 2005; Hruday 2011), but at present *E. coli* appears to provide the best bacterial indication of fecal contamination in DW (WHO 2008). This is based on the following: (a) the prevalence of thermotolerant (fecal) coliforms in temperate environments as compared to the rare incidence of *E. coli*; (b) the prevalence of *E. coli* in human and animal feces and generally not elsewhere in the environment; and (c) the availability of affordable, fast, sensitive, specific and easier test methods to detect *E. coli*.

Therefore, *E. coli* is the best and commonest microbial indicator available to date to inform public health risks associated with the consumption of contaminated DW (Staradumskyte & Paulauskas 2012; Odonkor & Ampofo 2013). Several European and American countries included this organism in their regulations as a primary indicator of fecal contamination in DW. Further, new data have shown that *E. coli* can also survive for an extended period of time in lake sediments (Byappanahalli *et al.* 2003).

## Fecal streptococci, enterococci or intestinal enterococci

Fecal streptococci, enterococci and intestinal enterococci are the three synonyms used to describe the members of genus *Enterococcus* comprising different species of sanitary significance. However, the survival characteristics and the proportions of the species of this group are not the same in animal and human feces (Borrego *et al.* 2002b; Figueras *et al.* 2008). It is advantageous to use these microorganisms as a useful indicator of the microbiological quality of DW because: (a) they show a close relationship with the health risks due to the consumption of contaminated DW, mainly for gastrointestinal symptoms; (b) they are always present in the feces of warm-blooded animals; (c) their inability to multiply in sewage-contaminated water resources; (d) they are not ubiquitous as coliforms; and (e) their die-off rate is slower than that of coliforms in water as well as their persistence pattern being similar to that of potential waterborne bacterial pathogens (Figueras *et al.* 2008; Layton *et al.* 2010).

## Alternative IMs

The traditional microbial indicators proposed by various researchers have presented several shortcomings and they cannot be used in all water types. In this instance, other indicators named 'alternative', should be used to determine the possible threats to the public health (Figueras *et al.* 2000; WHO 2004, 2008).

## Sulfite-reducing clostridia

The genus *Clostridium* (*C. perfringens*) as an indicator of fecal contamination and sanitary quality of water is based on the following assumptions (WHO 2008; Figueras *et al.* 2008):

- the presence of these microorganisms in the feces of all warm-blooded animals as well as in sewage;
- more stability in environmental water and greater resistance to disinfection processes than most pathogens;
- successful use in the monitoring of sewage contamination in water (Figueras *et al.* 2000; WHO 2004, 2008).

Nevertheless, the sulfite-reducing clostridia are considered ubiquitous in aquatic sediments and their spores are highly resistant to environmental stress. This explains

their long-term persistence in environmental water compared to other fecal indicator bacteria (Horman *et al.* 2004; Zheng *et al.* 2013), although they can also be used as indicators of remote or old fecal contamination (Desmarais *et al.* 2002) or to evaluate the virus/cyst inactivation in DW by disinfection methods (Figueras *et al.* 2000; Chauret *et al.* 2001; Borrego *et al.* 2002a; Viau & Boehm 2011; Vierheilig *et al.* 2013). However, WHO (2008) does not recommend the routine monitoring of distribution systems for the presence of clostridia due to their long period of survival and because they can be detected long after as well as far from the contamination site, leading to possible false signals.

### Bifidobacterium

*Bifidobacterium* spp. is one of the most numerous and extremely variable groups of bacteria present in the feces of warm-blooded animals (Bonjoch *et al.* 2004; Wilson 2005). The genus contains 25 spp., most of which have been detected in the human gastrointestinal tract (GI-tract) (Sinton *et al.* 1998; Biavati & Mattarelli 2003; Wilson 2005).

Bifidobacteria are present in high numbers in the feces of humans and some animals. Several *Bifidobacterium* species are specific either for humans or for animals. *Bifidobacterium cuniculi* and *B. magnum* have only been found in rabbit fecal samples, *B. gallinarum* and *B. pullorum* only in the intestines of chickens and *B. suis* only in piglet feces. In human feces, the species composition changes with the age of the individual. In the intestines of infants, *B. breve* and *B. longum* generally predominate. In adults, *B. adolescentis*, *B. catenulatum*, *B. pseudocatenulatum* and *B. longum* are the dominant species. In both human and animal feces, bifidobacteria are always much more abundant than coliforms (Sinton *et al.* 1998; Biavati & Mattarelli 2003; Wilson 2005; Cabral 2010).

Bifidobacteria have been found in sewage and contaminated water but appear to be absent from decontaminated or pristine environments such as springs and decontaminated soils (Lamendella *et al.* 2008). This results from the fact that upon introduction into the environment, bifidobacteria decreases appreciably in numbers, probably due to their stringent growth requirements. Bifidobacteria grow poorly below 30 °C and have rigorous nutrient requirements. The reports available on the survival of bifidobacteria in environmental

waters indicate that their survival is lower than that of coliforms (Biavati & Mattarelli 2003; Wilson 2005).

A study carried out in a highly contaminated stream near Bologna, Italy, revealed that *B. adolescentis*, *B. catenulatum*, *B. longum*, *B. pseudocatenulatum* and *B. thermophilum* were the most representative species, whereas *B. angulatum*, *B. animalis* subsp. *animalis* (*B. animalis*), *B. breve*, *B. choerinum*, *B. minimum*, *B. pseudolongum* subsp. *globosum* (*B. globosum*) and *B. subtile* occurred only in low numbers (Wilson 2005; Cabral 2010).

Thus, the presence of bifidobacteria spp. in the water environment is considered as an indicator of fecal contamination of water because some species are specific to humans and animals (King *et al.* 2007; Wery *et al.* 2010; Cabral 2010) as well as the alternative water quality indicators in tropical and temperate areas (Stewart *et al.* 2008; Mushi *et al.* 2010). Therefore, the identification of bifidobacterium species from contaminated water could provide information about the origin of fecal contamination (Sinton *et al.* 1998; Biavati & Mattarelli 2003; Wilson 2005).

### Bacteroides

Bacteroides are among the most oxygen-tolerant microbes of the entire anaerobic microflora found in the human GI-tract. Till now, the need to maintain anoxic conditions for cultivation, isolation and biochemical identification has limited the use of anaerobic bacteroides species as a fecal indicator. The survival of bacteroides in water environments is usually much lower than that of coliforms (Wilson 2005; Cabral 2010). However, the increasing use of recent molecular methods overcomes this problem (Kreader 1995; Balleste & Blanch 2010) as certain bacteroides species are highly host-specific and it is now possible to identify the source of fecal contamination by tracking the host-specific bacteroides species (Bernhard & Field 2000; Simpson *et al.* 2004; Bonjoch *et al.* 2005; Field & Samadpour 2007; Sauer *et al.* 2011; Zheng *et al.* 2013).

### Genetic markers from fecal *Bacteroides* distinguishing the source of fecal pollution

To distinguish the source of fecal pollution in fresh and marine waters, a new polymerase chain reaction (PCR)-based

indicator system, utilizing molecular markers from the *Bacteroides* group of fecal anaerobic bacteria, has been developed (Field et al. 2003; Bower et al. 2005; Fogarty & Voytek 2005; Sauer et al. 2011). This method detects the genetic marker sequences that are not only specific to fecal bacteria but are also specific to the host species that produced the feces, allowing discrimination among different potential sources of pollution. Furthermore, this method does not require isolation and growth of the indicator bacteria and it is rapid and accurate. Conversely, samples can be stored before analysis if necessary or convenient since the analysis does not require living cells. This allows for convenient and flexible field handling. In addition, scoring does not require complex pattern interpretation. The utility of this method of fecal source discrimination depends on the range of applicability of the genetic markers. Markers represent particular related groups of fecal bacteria, found in one host organism but not another. The specific primers amplify a band, which indicates the specific type of fecal pollution, or if there is no band, it indicates that the specific source of fecal pollution is absent or present at a level below the detection limit.

Recently, the identification of human- and bovine-specific *Bacteroides-Prevotella* 16S rRNA genetic markers by using length heterogeneity-PCR and terminal-restriction fragment length polymorphism has been reported, and the conclusion is that these markers could be used to detect the human or bovine origin of fecal pollution (Bernhard & Field 2000; Zheng et al. 2013). Owing to these advantages, PCR detection of *Bacteroides* markers has emerged as a potential tool for fecal source-tracking studies in the USA (Bernhard et al. 2003), France (Gourmelon et al. 2007), UK, Portugal, Ireland (Gawler et al. 2007), Belgium (Seurinck et al. 2006), Japan (Okabe et al. 2006) and Australia (Ahmed et al. 2008). Real-time PCR methods have been developed and used to quantify the human-specific *Bacteroides* genetic markers in environmental samples (Okabe et al. 2006; Seurinck et al. 2006).

However, *Bacteroides* spp. generally survive up to 6 days under limited oxygen while the human-specific *Bacteroides* genetic marker could persist in freshwater for up to 8 days at 23 °C under laboratory conditions (Seurinck et al. 2005). Further, the die-off rate of *Bacteroides* spp. could be triggered by environmental factors such as temperature and predation (Rozen & Belkin 2001). A limitation of the

*Bacteroides* genetic markers is that the specificity must be assessed prior to application because horizontal transfer of fecal bacteria is possible among the species in close contact, such as humans and dogs (Dick et al. 2005).

## Bacteriophages

Bacteriophages have been proposed as an indicator of fecal and viral contamination and also as models to evaluate the chlorination efficiency of water treatment plants (Leclerc et al. 2000; Duran et al. 2003; Mendez et al. 2004). The proposed groups include somatic coliphages, F (male)-specific RNA bacteriophages (F-RNA phages) and phages of *Bacteroides fragilis* (Duran et al. 2003).

Somatic coliphages are specific to *E. coli* and have been commonly used as an indicator of fecal and/or sewage contamination in several water resources. These are also used as biotracers to identify the source of contamination in surface water and aquifers (Paul et al. 1995; Muniesa et al. 2012). In addition, they indicate the pathogen removal efficiency of WWTPs (Harvey 1997). Hence, on the basis of differences in origin and ecology between the enteric viruses and somatic coliphages, it is doubtful to conclude that this phage group could successfully be used in all the situations as enteric viruses (Havelaar & Pot-Hogbeem 1988). They also may not be a useful indicator of an integrity problem in a distribution system, even when the problem involves the introduction of fecal contamination (Hot et al. 2003).

F-RNA phages are used as an indicator of fecal contamination as well as model viruses in water hygiene because of: (a) similar size and shape to human enteric viruses; (b) direct correlation with degree of sewage contamination; and (c) inability to replicate in the water environment (Duran et al. 2003).

However, the low incidence of this phage group in human feces and its low specificity for its bacterial host has suggested that they would multiply in sewer systems (Cornax et al. 1994). Hence, the presence of F-RNA phages in water should be primarily used as an indicator of sewage contamination rather than fecal contamination (Scott et al. 2002; Hot et al. 2003). *Bacteroides fragilis*, a strict anaerobe, is found at high concentrations in the human intestinal tract and dies rapidly when discharged into the water environment. A phage of strain HSP 40 of *B. fragilis*, which



was isolated from Hospital San Pablo, Barcelona, Spain, has been reported as a specific indicator of human fecal contamination in the water environment (Duran *et al.* 2003) because: (a) the phages against this bacterial strain are human-specific and are not isolated from the feces of other homoeothermic animals; (b) *B. fragilis* HSP 40 phages are consistently isolated from the water contaminated with sewage and feces and their sediments, but not from the decontaminated samples; (c) the number of phages is related to the degree of contamination; (d) *B. fragilis* phages always outnumber the human enteric viruses; and (e) in model experiments, no replication of these phages has been observed under simulated environmental conditions (Leclerc *et al.* 2000).

Thus, the low prevalence to these phages in water with low or moderate levels of fecal contamination and complex methodology for their recovery are major drawbacks for the general use of these viruses as IMs (Cornax *et al.* 1991; Ashbolt *et al.* 2001; Miernik 2004).

### Heterotrophic plate counts

The total aerobic bacteria or heterotrophic plate count (HPC) were among the first parameters that were used in the late 1800s to assess the 'purity' of source water (Bartram *et al.* 2003; Maal-Bared *et al.* 2008). However, these are no longer used as health-related indicators (Edberg & Smith 1988; Verhille 2013). At present, they have become the general indicator of water quality within the DWDS (WHO 2004, 2008). Today, significant changes in HPC serve as an alert for possible deterioration of water quality, triggering further investigation (Bartram *et al.* 2003; Verhille 2013). An increase in HPC in treated water indicates the failure of the water treatment plant or a change in quality of the water source, prior to treatment (Bartram *et al.* 2003). If the HPC level in water leaving the treatment plant is acceptable, but it is high in the distribution system, it indicates that either the re-growth has taken place or it has been contaminated due to cracks/leakage in the distribution system (Bartram *et al.* 2003; Verhille 2013).

### Emerging waterborne bacterial pathogens

Emerging waterborne pathogens pose a major health hazard in both developed and developing countries. The rapid

emergence of waterborne pathogens has created a serious threat to DW safety. Hence, there is an urgent need to develop strategies for the identification of these potentially emerging waterborne pathogens. There may be several reasons for the continuous emergence of waterborne pathogens such as: (a) increase in sensitive populations; (b) globalization of trade and travel; (c) development of molecular techniques (MTs) for detection and source tracking; (d) changes in DW treatment technology; (e) changes in food production and supply; (f) molecular evolution (genetic reassortment); and (g) multi-drug resistance (Sharma *et al.* 2003; Nwachuku & Gerba 2004; Skovgaard 2007; Chugh 2008; Sherchand 2012; Morens & Fauci 2013). However, several microbial agents which may qualify as emerging waterborne pathogens have been reported by many authors (Sharma *et al.* 2003; Nwachuku & Gerba 2004; Health Canada 2006; Petrini 2006; Cohen *et al.* 2007; Skovgaard 2007; Cangelosi 2009; Cabral 2010; Adrados *et al.* 2011; Whiley *et al.* 2012). These include environmental mycobacteria, aeromonads (*Aeromonas sobria*, *A. caviae* and *A. hydrophila*), *Legionella pneumophila*, *Vibrio* sp. (*V. cholerae* O139 and *V. cholerae* O1), pathogenic *E. coli* (enteroinvasive *E. coli*, enteropathogenic *E. coli*, enteroaggregative *E. coli* and shiga toxin producing *E. coli*), *Yersinia enterocolitica*, *Helicobacter pylori*, multidrug resistant *Pseudomonas aeruginosa* and *Campylobacter jejuni*. These pathogens have the potential to be spread through the supply of DW. However, their presence does not correlate with the presence of *E. coli* or other microbial indicators. In most cases there are no perfect microbial indicators to indicate the presence of emerging waterborne pathogens. The development of microbial source tracking (MST) has allowed the identification of sources of these waterborne pathogens (Noble *et al.* 2003; Gao *et al.* 2008; Beumer *et al.* 2010; Adrados *et al.* 2011; Furtula *et al.* 2012; Zheng *et al.* 2013). However, more studies are required to understand the behavior and ecology of these waterborne pathogens so that their true potential as emerging waterborne pathogens may be evaluated.

### Fecal sterol biomarkers as alternative indicators of fecal pollution

The detection of pathogens still depends on the development of more flexible and reliable techniques. In addition,

most of the IMs are not suitable for monitoring the level of fecal pollution in tropical and temperate environments because they could multiply or be a part of natural flora (Savichtcheva & Okabe 2006). Therefore, certain fecal organic compounds such as fecal sterols could be used as an alternative indicator of fecal contamination (Isobe *et al.* 2002, 2004; Furtula *et al.* 2012; Zheng *et al.* 2013). Coprostanol (5 $\beta$ -cholestan-3 $\beta$ -ol) is one of the major fecal sterols produced by indigenous bacteria (normal microflora) present in human and animal intestines and excreted in feces (Cabral 2010). Under aerobic conditions, coprostanol can be microbially degraded in the water column and has a half-life of less than 10 days at 20 °C (Isobe *et al.* 2002). It indicates the presence of microbes in water environments and its measurement has been proposed as a powerful tool for monitoring fresh fecal contamination in tropical regions of Japan, Malaysia and Vietnam (Isobe *et al.* 2002, 2004; Ashbolt *et al.* 2007; Derriena *et al.* 2012). However, a sensitive and simple analytical method using gas chromatography–mass spectrometry has been successfully developed for various environmental samples (Isobe *et al.* 2002; Savichtcheva & Okabe 2006).

Since coprostanol is hydrophobic, it is readily associated with sewage and water particles. Fecal sterols could, therefore, be incorporated into sediments and preserved for a long time under anoxic conditions without significant biodegradation (stable for 450 days at 15 °C) (Isobe *et al.* 2002). All these facts explain the findings that coprostanol was also found far from the possible fecal pollution source. Therefore, the presence of coprostanol mainly in sediments may indicate old or remote fecal pollution (Savichtcheva & Okabe 2006). In addition, lack of studies on application of host specificity, and desirable detection sensitivity and correlation with pathogens limit current application of fecal sterols on a large scale and indicate the need for future investigations.

### Recovery of injured bacteria

Many indicator bacteria may become damaged during the water and wastewater treatment process due to the sub-lethal exposure to a wide variety of chemical/physical agents (Toranzos *et al.* 2007; Cordoba *et al.* 2010; Kahlisch *et al.* 2010). These injured bacteria are unable to form

colonies on selective media and ~90% of indicator bacteria in treated DW may be damaged (McFeters 1990). As a consequence, the injured cells remain undetected in water leading to the underestimation of fecal contamination levels in treated DW in distribution systems (Bucklin *et al.* 1991). The abilities of several methods to detect the damaged bacteria were reviewed earlier by various workers (WHO 2004, 2008; Kahlisch *et al.* 2010). The detection of damaged bacteria in the distribution system may be an indication of either re-growth of damaged bacteria in the presence of high level of nutrients or contamination due to cracks/leakage in the distribution system. Thus, it may provide guidelines to diagnose the problems within the water distribution system (Toranzos *et al.* 2007).

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## TECHNIQUES FOR THE DETECTION OF INDICATOR AND PATHOGENIC MICROORGANISMS IN WATER ENVIRONMENTS

A significant number of human microbial pathogens are present in urban sewage and may be considered as environmental pollutants. Although most of the pathogens can be removed during the wastewater treatment, many are discharged into wastewater and entering and receiving waters. Point-source pollution enters the environment at distinct locations, through a direct route of discharge of treated and untreated wastewater. Non-point sources of pollution are of significant concern with respect to the spread of pathogens and their indicators in water environments.

Traditional microbial indicators viz. FCs, *E. coli* and enterococci are the most commonly used IMs. These are analyzed to evaluate the level of fecal contamination in water environments and are also used to assess the pathogen removal efficiency of water treatment plants. However, whether these bacteria are suitable indicators of human pathogens has been questioned (Tree *et al.* 2003; Wery *et al.* 2008). There are several limitations in the general use of indicator bacteria as water quality indicators such as they are sensitive to inactivation during treatment processes and also by sunlight exposure (Hurst *et al.* 2002; Sinclair *et al.* 2009), short survival as compared to pathogens (McFeters *et al.* 1974), non-exclusive fecal sources (Scott *et al.* 2002; Simpson *et al.* 2002), ability to

multiply in some natural environments (Solo-Gabriele *et al.* 2000; Pote *et al.* 2009), inability to identify the source of fecal pollution (point or non-point) (Field *et al.* 2003) and bad correlation with the presence of pathogenic microorganisms (Horman *et al.* 2004; Savichtcheva & Okabe 2006). Culturing the pathogens in laboratories is also a laborious process that involves culture enrichment and selective media for the isolation of pathogens from the background organism. It is often difficult to achieve the appropriate culture enrichment, which makes the work even more tedious. Moreover, the concentrations of pathogens may be too low for the culture detection but still potent enough to cause disease. As a result, there are no ideal bacterial indicators currently used that fulfill all the established criteria for drinking or bathing water quality. Thus, the direct detection of pathogens of health concern without culturing in laboratories but with the help of MTs is considered to be a more suitable alternative (Gilbride *et al.* 2006) (Table 7).

The MTs, particularly nucleic acid amplification methods, provide sensitive, rapid and quantitative means for detecting the specific pathogens of public health and environmental concern including new emergent bacterial strains and indicators. These techniques are used to evaluate the microbiological quality of water and pathogens removal efficiency from DW and WWTPs. These techniques are together regarded as MST or bacterial source-tracking. These MTs aim to identify, and in some cases quantify, the dominant fecal contamination sources in the environment, and more particularly in water resources (Fong & Lipp 2005; Hundesa *et al.* 2006; Albinana-Gimenez *et al.* 2009). These MTs allow researchers to rapidly and specifically detect the microorganisms of public health and environmental concern, although recent improvements have allowed the simultaneous detection of several or groups of microorganisms in a single assay (Maynard *et al.* 2005; Straub *et al.* 2005; Marcelino *et al.* 2006). These developments have allowed the potential standardization and automation of some of these techniques. In some cases, these facilitate the identification, enumeration, genotyping, viability assessment and source-tracking of the fecal pollution of human or animal origin, if host-specific, most prevalent pathogens are analyzed. The MTs available today are being

continuously improved in order to make them standardized and applicable to a wide variety of matrices, to increase their sensitivity, rapidity and to reduce the time, costs and steps used for the detection of pathogens and indicators. The standardization and validation of protocols is considered critical for the implementation of MTs used in the clinical or environmental area and has a potential impact on the evaluation of the data produced in many studies (Doring *et al.* 2008; Raymaekers *et al.* 2009; Harwood *et al.* 2009; Bustin 2010).

### Assessing the viability of pathogenic microorganisms

A number of pathogenic bacteria can be found in the environmental media (air, water and soil). Therefore, it is important to assess the viability status of these organisms to determine whether or not they pose a serious threat to public health. The conventional methods available for the determination of bacterial viability are based on the ability of cells to grow actively and form visible colonies on solid media. Moreover, under certain conditions the number of viable organisms may be severely underrepresented by such methods as sublethally damaged organisms (Blackburn & McCarthy 2000), fastidious unculturable bacteria (Ward *et al.* 1990) and viable cells that have lost their ability to form colonies under test conditions. These conventional methods are laborious and time consuming. Therefore, MTs have been developed as an alternative to overcome the limitations of conventional methods. These MTs offer speed, sensitivity and specificity wherein both the DNA and RNA have been analyzed using nucleic acid amplification methods such as PCR, reverse transcriptase-PCR and nucleic acid sequence-based amplification. However, due to the variable persistence of nucleic acids in the cells after death, the correlation between the presence of DNA and RNA and viability is not clear. Similarly, the choice of target and sensitivity of the methods used to assess the bacterial viability can significantly affect the validity of the viability assays. However, the accuracy of such methods is greatly dependent on both the manner of cell death and environmental conditions. Further, detailed information on assessing bacterial viability can be found in the review article entitled 'Molecular methods for the assessment of bacterial viability' (Keer & Birch 2003).

**Table 7** | Techniques for the detection of pathogens and indicators from water, wastewater and other environmental samples

Technique	Merit	Demerit
Conventional techniques		
Microscopy	Simple, rapid and direct observation of microbial cells	Majority of bacterial population cannot be identified
Culture-dependent methods	Easy to identify the individual microbes	Majority of bacteria cannot be cultured on the general purpose-basic media
Microbial indicator-based pathogen estimation	Easy to perform, current standard for coliform has been established	Labor intensive, time consuming and indirect estimation of pathogens rather than direct detection
Molecular techniques		
Ribotyping	Highly reproducible; classify isolates from multiple sources	Complex, expensive; labor intensive; geographically specific; database required; variation in methodology
Amplified ribosomal DNA restriction analysis (ARDRA)	Culture-independent technique and suitable for analysis of a variety of microbes	Not quantitative and require DNA extraction and PCR biases
Ribosomal RNA intergenic spacer analysis (RISA)	Culture-independent technique, suitable for analysis of a variety of microbes and give remarkable heterogeneity in length and sequence among bacteria	Not quantitative and require DNA extraction and PCR biases
Pulse-field gel electrophoresis (PFGE)	Extremely reproducible and highly sensitive to point genetic difference	Long assay time, too sensitive for broadly discriminate source, limited simultaneous processing and required database
Denaturing-gradient gel electrophoresis (DGGE)	Culture-independent technique, suitable for analysis of a variety of microbes and use rRNA gene sequence heterogeneity	DNA extraction and PCR biases
Terminal-restriction fragment length polymorphism analysis (T-RFLP)	Fast, semi-quantitative, culture-independent technique and suitable for analysis of a variety of microbes	DNA extraction and PCR biases
Fluorescent <i>in situ</i> hybridization (FISH)	Quantitative and directly visualize the microbial cells including non-culturables	Inactive cells may not be detected
Quantitative PCR (qPCR)	Culture-independent technique and suitable for analysis of a variety of microbes	Expensive equipment; technically demanding
Repetitive DNA sequences (Rep-PCR)	Simple and rapid	Reproducibility a concern; cell culture required; large database required; variability increases as database increases
Length heterogeneity-PCR (LH-PCR)	Culture-independent technique	Expensive equipment; technically demanding
Multiplex PCR (mPCR)	Fast and simultaneous detection of several target microorganisms	Combination of primer pairs must function in a single PCR reaction
Nucleic acid microarrays	High throughput design with wider applications	Low sensitivity and processing complexities for environmental samples
Host-specific 16S rDNA	Does not require culturing or a database; indicator of recent pollution	Only tested on human and cattle markers; limited simultaneous processing; expensive equipment; technically demanding; little information about survival of <i>Bacteroides</i> spp. in environment
On-chip technology	Combination of PCR with nucleic acid hybridization on a single chip and less interference between parallel reactions	Integration and packaging

Adapted from Simpson *et al.* (2002), Scott *et al.* (2002), Meays *et al.* (2004), Gilbride *et al.* (2006) and Girones *et al.* (2010).

## DRINKING WATER QUALITY STANDARDS AND GUIDELINES

At present, microbial indicators that are being used to monitor the microbiological quality of DW in developed countries are TCs, FCs and/or *E. coli*, although the reliance on IMs as the main source of information about the safety of DW is under review in many jurisdictions (Ashbolt *et al.* 2001; WHO 2008; Health Canada 2013) (Table 8).

### WHO guidelines and WSPs

The WHO has recommended WSPs for consistently ensuring the supply of safe DW. These safety plans manage the risk from the catchment or water source to the consumer's home (WHO 2004, 2008; Bartram *et al.* 2009). The risk assessment included in WSP should provide a better understanding of the risks associated with water contamination at each step along with the distribution system. Therefore, the preventive strategies should be designed (a multi-barrier protection system) in order to correctly manage these risks efficiently and effectively to protect the public health. This approach does not rely solely on end-point testing, but on the establishment of critical control points that will be subject to on-line monitoring. The parameters that can be measured on-line and in real-time are free chlorine, water pressure, dissolved oxygen and turbidity to which critical safety limits are established. In this way, any sudden anomalous changes in any of these parameters may indicate a problem within the distribution system that can be managed before the water is supplied to the consumers.

The introduction of these early warning or control parameters from source to consumer's home that can predict or alert the possible deterioration of DW quality before it is distributed to the consumers are the key elements of WSPs. Analyzing the DW microbiologically, for the enumeration and identification of IMs, is too slow (i.e., requires minimum of 24–48 h) and, therefore, is not suitable. However, they play an important role as validation tools because they verify whether the barriers work properly and the whole process is under control. In reality, many large water companies have long been adopting the principles of risk assessment and risk management, mostly in

the form of operational procedures, for the treatment processes and distribution networks. Therefore, the adoption of these approaches will not be difficult, but beneficial as already reported (Gunnarsdóttir & Gissurarson 2008). In the EU research-financed project (Healthy Water), one of the objectives was to train the water companies on the principles of WSPs, and experience has demonstrated that companies acknowledged the benefit of the new approaches; some of the largest water companies have already incorporated it.

However, small water companies will only implement the WSPs, when the approaches become a mandatory requirement under new EU legislation. In reality, the legislation is the driving force for such improvements, as outlined previously. For instance, the National Spanish Legislation on *Legionella*, promulgated after the world's largest outbreak, requires a part of the microbiological control with two other obligations:

- (i) to pass a training course for those who are responsible for handling the installations at risk of propagating the legionellosis;
- (ii) to implement the control plans based on the methodology of HACCP.

Further, according to Bartram *et al.* (2004), health care facilities should have general WSPs as an important part of their infection control strategies. Such plans may be generic (i.e., applicable to health centers in general) or specific for larger buildings (i.e., hospitals and nursing homes) and should address microbial growth in addition to control of external contamination by *P. aeruginosa* and *Legionella*, etc.

The WSPs have to be developed by a team and require:

- specific measures to protect raw water used to produce DW (i.e., fencing);
- the appropriate level of treatment in water companies as well as during the storage and distribution through pipe networks to customer's homes to guarantee the quality of DW;
- that customers are aware of their role and responsibilities for keeping the water as wholesome as possible in their properties, which include both public buildings as well as private homes.

**Table 8** | International DW standards or guidelines

Parameters	Canada	United States	Australia	New Zealand	United Kingdom	EU Directive	WHO	India	Middle East	South Africa	South America
Guidelines or standards	G <sup>a</sup>	S	G	S <sup>b</sup>	S	S	G	G	G	G	S <sup>c</sup>
Total coliforms	0/100 mL in 90%	0/100 mL <sup>d</sup> in 90%	0/100 mL in 95%		0/100 mL (s)	0/100 mL		3/100 mL <sup>e</sup> in 95%	0/100 mL		≤3/100 mL in 95%
Thermotolerant coliforms or <i>E. coli</i>		0/100 mL	0/100 mL in 98%				0/100 mL	0/100 mL		<1/100 mL	0/100 mL in 95%
<i>E. coli</i>		0/100 mL	0/100 mL <sup>f</sup>	0/100 mL	0/100 mL(t)	0/100 mL	0/100 mL <sup>g</sup>	0/100 mL		0/100 mL	0/100 mL
Enterococci					0/100 mL(t)	0/100 mL					
<i>Cryptosporidium parvum</i>		995 removal or inactivation			<1 Oocyte/10 mL						
<i>Clostridium perfringens</i> with spores					0/100 mL	( <sup>h</sup> )					
<i>Pseudomonas aeruginosa</i>						0/250 mL <sup>i</sup>					
Colony count 22 °C					No abnormal change	No abnormal change					
Colony count 37 °C	<500 cfu/mL <sup>j</sup>				No abnormal change	20/mL <sup>i</sup>			10 to <100 cfu/mL <sup>j</sup>		<500 cfu/mL <sup>j</sup>

Adapted from DWAF (1996), Tallon *et al.* (2005), Tyagi *et al.* (2006), WHO (2008) and Pinto *et al.* (2012).

Spaces left blank indicate parameters that are not specified. All values are CFU/100 mL (colony forming units) unless otherwise stated. EU – European Union (includes Austria, Belgium, Denmark, Finland, France, Germany, Greece, Ireland, Italy, Luxembourg, Netherlands, Portugal, Spain, Sweden, United Kingdom of Great Britain and Northern Ireland. Ten countries joined the EU on 1 May 2004: Cyprus (Greek part), the Czech Republic, Estonia, Hungary, Latvia, Lithuania, Malta, Poland, Slovakia and Slovenia.) WHO – World Health Organization, G – guidelines, S – standards, HPC – heterotrophic plate count.

\*Data are based on literature published before 2004.

<sup>a</sup>Alberta, Quebec and British Columbia have standards.

<sup>b</sup>New Zealand has non-enforceable standards and has made the decision to use only *E. coli*.

<sup>c</sup>Standards in the following countries of South America: Argentina, Bolivia, Brazil, Chile, Colombia, Ecuador, Paraguay, Peru, Uruguay and Venezuela.

<sup>d</sup>A coliform positive sample requires repeat sampling within 24 h. If this repeat sample is also coliform-positive then it must be tested for fecal coliforms and *E. coli*. A positive result for this test requires notification of appropriate authorities.

<sup>e</sup>In an occasional sample, but not in consecutive samples.

<sup>f</sup>Recommends that *E. coli* be retained as the primary compliance parameter for fecal contamination.

<sup>g</sup>Recognizes that *E. coli* is the preferred indicator of fecal contamination.

<sup>h</sup>Necessary only if the water originates from or is influenced by surface water.

<sup>i</sup>Necessary only in the case of water offered for sale in bottles or containers.

<sup>j</sup>HPC (35 °C for 48 h) or <200 background coliforms on a total coliform membrane filter. '<' indicates less than.

Protection of the entire catchment areas is the first step of multiple barrier protection concepts. Modeling can be used for establishing the microbial risks in DW catchments and can also be an excellent management tool in the development of WSP (Gunnarsdottir & Gissurarson 2008). There is much evidence indicating that inappropriate water handling is an important source of water contamination at the consumer's home. Considering this, the WHO has prepared a specific manual for the management of the microbiological quality of DW in a piped distribution system. Further, the information on how to implement the WSP can be found in WHO technical guidance documents including the WSP manual (Bartram *et al.* 2009) in which many specific case studies are presented. A dedicated website on the WSPs has also been developed by the 'IWA' ([www.wsportal.org/ibis/water-safety-portal/eng/welcome](http://www.wsportal.org/ibis/water-safety-portal/eng/welcome)). In addition, the WHO and the IWA have developed guiding documents to initiate such processes considering all levels of resources available, so that they can be implemented all over the world, even in poorly developed countries.

### Strategies minimizing waterborne illness outbreaks in developing countries

In developing countries, the following strategies are used as low-cost alternatives, which are effective in preventing the spread of WBDs (WHO 2007).

#### Chlorination

It is a widely used method for water purification wherein chlorine (a disinfectant) is added in liquid or tablet form to kill the pathogenic microorganisms present in DW supply reservoirs. Therefore, water that has been treated with chlorine is effective in preventing the spread of WBDs.

#### Boiling

It is the oldest and most commonly used effective approach to disinfect water at a household level that kills most of the microbes causing intestine-related diseases.

#### Solar disinfection

It is a type of portable water purification systems (self-contained units) that is also known as point-of-use water treatment. In this method, the clear DW in disposable clear plastic bottles is exposed to sunlight for a day. Principally, it is the combined action of heat and UV light received from the sun that is used to inactivate the pathogens present in water.

#### Filtration

It is used to purify water through high-quality ceramic filters with small pores, often coated with silver, which has been shown to be effective in removing many microbes and other suspended solid particles. These devices can be directly installed at water outlets in order to protect users against potentially harmful waterborne pathogens by providing a barrier to them and/or minimizing patient exposure. To be effective, filters need to be cleaned regularly to maintain the flow of water.

#### Combined flocculation/disinfection systems

It is the addition of chlorine in powder or tablet form to coagulate and flocculate the sediments present in water followed by a timed release of disinfectant (chlorine). It is particularly used for the treatment of turbid water. The water is normally stirred for few minutes, strained to separate the flocculants and then allowed to stand for another half hour for the complete disinfection process.

#### Safe storage

It has been shown that water that is safe at the point of collection is often subject to fecal contamination during the collection, transport and use at home, mainly by unclean hands. Many studies have also shown that vessels with narrow mouths and taps can significantly reduce such contamination and reduce the risk of DDs. Wherever possible, safe storage should also be included in the interventions to treat the water at home.

## Future implications for international guidelines and national regulations

Traditionally, the indicators have played a crucial role in implementing the guidelines and national standards. However, these are being seen as an adjunct to management controls such as sanitary surveys and there is a move away from a specified indicator level end product. In other words, indicators are being replaced by on-line analyzes (say for chlorine residual or particle sizes) at critical control points. A single indicator, or even a range of indicators, is unlikely to be appropriate for every occasion and, therefore, it is useful to tailor indicator choice to local circumstances when translating the international guidelines into national standards. In addition, with the change in the management paradigm, more indicators of process efficiency are required rather than reliance on the 'old-style' fecal indicators.

## CONCLUSIONS

- (a) The availability of safe DW for all is one of the major challenges of the 21st century.
- (b) The microbiological control of DW should be the norm everywhere.
- (c) An adequate, safe and accessible supply of DW must be available to all.
- (d) Routine basic microbiological analysis of DW should be carried out for the presence of *E. coli* by culture-dependent methods. On-line monitoring of glucuronidase activity is currently too insensitive to replace the culture-based detection of *E. coli*, but it is a valuable complementary tool for high temporal resolution monitoring. Whenever the financial resources are available, coliform determinations should be complemented with the quantification of enterococci.
- (e) Financial resources should be devoted to the better understanding of sources of microbial contaminants (human versus animal), their transport, prevalence and fate in water environments. The health risks posed by these microbial contaminants also needs to be investigated.
- (f) The development of alternative fecal indicators to replace or to combine with conventional ones requires

additional adequate investigation and an epidemiological survey of their applications.

- (g) The techniques available for direct detection of pathogens/microbial indicators require improvement in order to make them standardized and of wider application, but further research and evolution of new methods are still needed.
- (h) More studies are required in order to understand the behavior and ecology of waterborne pathogens so that their true potential as emerging waterborne pathogens may be evaluated.

Thus, in conclusion we can say that there is no universal IM, but a number of microorganisms each with certain characteristics are being used as an indicator of the microbiological quality of DW. Therefore, this review article has mainly focused on elucidating the appropriate use of microbes as IMs with a view to their role in the management of waterborne microbial risks.

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## REFERENCES

- Adrados, B., Codony, J. E., Torrents, E., Luguin, M. & Morato, J. 2011 Prevalence and concentration of non-tuberculous mycobacteria in cooling towers by means of quantitative PCR: a prospective study. *Curr. Microbiol.* **62**, 313–319.
- Ahmed, W., Stewart, J., Powell, D. & Gardner, T. 2008 Evaluation of bacteroides markers for the detection of human fecal pollution. *Lett. Appl. Microbiol.* **46**, 237–242.
- Albinana-Gimenez, N., Miagostovich, M., Calgua, B., Huguet, J. M., Matia, L. & Girones, R. 2009 Analysis of adenoviruses and polyomaviruses quantified by qPCR as indicators of water quality in source and drinking water-treatment plants. *Water Res.* **43**, 2011–2019.
- American Water Works Association (AWWA) 1999 *Waterborne Pathogens*. 1st edn, AWWA, Washington, DC.



- Arnone, R. D. & Walling, J. P. 2007 [Waterborne pathogens in urban watersheds](#). *J. Water Health* **5** (1), 149–162.
- Ashbolt, N., Fujioka, R., Glymph, T., McGee, C., Schaub, S., Sobsey, M. & Toranzos, G. 2007 [Pathogen Indicators and Indicators of Fecal Contamination](#). Environmental Protection Agency, Office of Water, Office of Research and Development, Warrenton, VA, Chapter 2, pp. 35–56.
- Ashbolt, N. J., Grabow, O. K. & Snozzi, M. 2001 [Indicators of microbial water quality](#). In: *Water Quality: Guidelines, Standards and Health* (L. Fewtrell & J. Bartram, eds). IWA Publishing, London, UK, pp. 289–316.
- Ashbolt, N. J. 2004 [Microbial contamination of drinking water and disease outcomes in developing regions](#). *Toxicology* **198**, 229–238.
- Balleste, E. & Blanch, A. R. 2010 [Persistence of Bacteroides species populations in a river as measured by molecular and culture techniques](#). *Appl. Environ. Microbiol.* **76**, 7608–7616.
- Bartram, J., Cotruvo, J., Exner, M., Fricker, C. & Glasmacher, A. 2003 [Heterotrophic Counts and Drinking-water Safety: The Significance of HPCs for Water Quality and Human Health](#). IWA Publishing, London, UK.
- Bartram, J., Cotruvo, J., Exner, M., Fricker, C. & Glasmacher, A. 2004 [Heterotrophic plate count measurement in drinking water safety management](#). *Int. J. Food Microbiol.* **92**, 241–247.
- Bartram, J., Corrales, L., Davison, A., Deere, D., Drury, D., Gordon, B., Howard, G., Rinehold, A. & Stevens, M. 2009 [Water Safety Plan Manual: Step-by-Step Risk Management for Drinking Water Suppliers](#). World Health Organization, Geneva, Switzerland.
- Bernhard, A. E. & Field, K. G. 2000 [A PCR assay to discriminate human and ruminant feces on the basis of host differences in Bacteroides-Prevotella genes encoding 16S rRNA](#). *Appl. Environ. Microbiol.* **66** (10), 4571–4574.
- Bernhard, A. E., Goyard, T., Simmonich, M. T. & Field, K. G. 2003 [Application of a rapid method for identifying fecal pollution sources in a multi-use estuary](#). *Water Res.* **37**, 909–913.
- Beumer, A., King, D., Donohue, M., Mistry, J., Covert, T. & Pfaller, S. 2010 [Detection of Mycobacterium avium subsp. Paratuberculosis in drinking water and biofilms by quantitative PCR](#). *Appl. Environ. Microbiol.* **76** (21), 7367–7370.
- Biavati, B. & Mattarelli, P. 2003 [The family of bifidobacteriaceae](#). In: *The Prokaryotes. An Evolving Electronic Resource for the Microbiological Community* (M. Dworking, ed.). 3rd edn, Springer-Verlag, New York, pp. 3–14.
- Blackburn, C. W. & McCarthy, J. D. 2000 [Modifications to methods for the enumeration and detection of injured Escherichia coli O157:H7 in foods](#). *Int. J. Food Microbiol.* **55**, 285–290.
- Bonjoch, X., Balleste, E. & Blanch, A. R. 2005 [Enumeration of bifidobacterial populations with selective media to determine the source of water-borne fecal pollution](#). *Water Res.* **39**, 1621–1627.
- Bonjoch, X., Balleste, E. & Blanch, A. R. 2004 [Multiplex PCR with 16S rRNA gene-targeted primers of Bifidobacterium spp. to identify sources of fecal pollution](#). *Appl. Environ. Microbiol.* **70**, 3171–3175.
- Borrego, J. J., Castro, D. & Figueras, M. J. 2002a [Fecal streptococci/enterococci in aquatic environments](#). In: *Encyclopedia of Environmental Microbiology* (G. Bitton, ed.). John Wiley & Sons, New York, USA, pp. 1264–1278.
- Borrego, J. J., Castro, D. & Figueras, M. J. 2002b [Salmonella in aquatic environments](#). In: *Encyclopedia of Environmental Microbiology* (G. Bitton, ed.). John Wiley & Sons, New York, NY, USA, pp. 2789–2802.
- Bower, P. A., Scopel, C. O., Jensen, E. T., Depas, M. M. & McLellan, S. L. 2005 [Detection of genetic markers of fecal indicator bacteria in Lake Michigan and determination of their relationship to Escherichia coli densities using standard microbiological methods](#). *Appl. Environ. Microbiol.* **71** (12), 8305–8313.
- Bucklin, K. E., McFeters, G. A. & Amirtharaja, A. 1991 [Penetration of coliforms through municipal drinking water filters](#). *Water Res.* **25**, 1013–1017.
- Bustin, S. A. 2010 [Why the need for qPCR publication guidelines? The case for MIQE](#). *Methods* **50** (4), 217–226.
- Byappanahalli, M., Fowler, M., Shively, D. & Whitman, R. 2003 [Ubiquity and persistence of E. coli in a midwestern coastal stream](#). *Environ. Microbiol.* **69**, 4549–4555.
- Cabral, J. P. S. 2010 [Water microbiology. Bacterial pathogens and water](#). *Int. J. Environ. Res. Public Health* **7**, 3657–3703.
- Cangelosi, G. A. 2009 [Prospects for applying virulence factor-activity relationship \(VFAR\) to emerging waterborne pathogens](#). *J. Water Health* **7**, S64–S74.
- Chauret, C. P., Radzimiski, C. Z., Lepull, M., Creason, R. & Andrews, R. C. 2001 [Chlorine dioxide inactivation of Cryptosporidium parvum oocysts and bacterial spore indicators](#). *Appl. Environ. Microbiol.* **67**, 2993–3001.
- Chugh, T. D. 2008 [Emerging and re-emerging bacterial diseases in India](#). *J. Biosci.* **33**, 549–555.
- Clark, J. A. 1990 [The presence-absence tests for monitoring water quality](#). In: *Drinking Water Microbiology* (G. A. McFeters, ed.). Springer-Verlag, New York, pp. 399–411.
- Cohen, A. L., Oliver, J. D., DePaola, A., Feil, E. J. & Fidelma Boyd, E. 2007 [Emergence of a virulent clade of Vibrio vulnificus and correlation with the presence of a 33-kilobase genomic island](#). *Appl. Environ. Microbiol.* **73** (17), 5553–5565.
- Collado, L., Kasimir, G., Perez, U., Bosch, A., Pinto, R., Saucedo, G., Huguet, J. M. & Figueras, M. J. 2010 [Occurrence and diversity of Acrobacter spp. along the Llobregat River catchment at sewage effluents and in a drinking water treatment plant](#). *Water Res.* **44**, 3696–3702.
- Cordoba, M. A., Del Coco, V. F., Minvielle, M. C. & Basualdo, J. A. 2010 [Influencing factors in the occurrence of injured coliforms in the drinking water distribution system in the city of La Plata, Argentina](#). *J. Water Health* **8**, 205–211.
- Cornax, R., Morinigo, M. A., Balebona, M. C., Castro, D. & Borrego, J. J. 1991 [Significance of several bacteriophages groups as indicators of sewage pollution in marine waters](#). *Water Res.* **25**, 673–678.

- Cornax, R., Morinigo, M. A., Gonzalez-Jaen, F., Alonso, M. C. & Borrego, J. J. 1994 Bacteriophages presence in human faeces of healthy subjects and patients with gastrointestinal disturbances. *Zentbl. Bakteriol.* **281**, 214–224.
- Department of Water Affairs and Forestry (DWAF) 1996 *South African Water Quality Guidelines*. 2nd edn, Vol. 1: Domestic Use. CSIR Environmental Services. Pretoria. Republic of South Africa. Available from: [www.dwaf.gov.za/IWQS/wq\\_guide/domestic.pdf](http://www.dwaf.gov.za/IWQS/wq_guide/domestic.pdf).
- Derriena, M., Jardea, E., Gruaua, G., Pourcherb, A. M., Gourmelon, M., Jadas-Hécartd, A. & Pierson Wickmanna, A. C. 2012 Origin of fecal contamination in waters from contrasted areas: stanols as microbial source tracking markers. *Water Res.* **46** (13), 4009–4016.
- Desmarais, T. R., Solo-Gabriele, H. M. & Palmer, C. J. 2002 Influence of soil on fecal indicator organisms in a tidally influenced subtropical environment. *Appl. Environ. Microbiol.* **68**, 1165–1172.
- Dick, L. K., Bernhard, A. E., Brodeur, T. J., Santo Domingo, J. W., Simpson, J. M., Walters, S. P. & Field, K. G. 2005 Host distributions of uncultivated fecal Bacteroidales bacteria reveal genetic markers for fecal source identification. *Appl. Environ. Microbiol.* **71**, 3184–3191.
- Doring, G., Unertl, K. & Heining, A. 2008 Validation criteria for nucleic acid amplification techniques for bacterial infections. *Clin. Chem. Lab. Med.* **46**, 909–918.
- Dufour, A., Snozzi, M., Koster, W., Bartram, J., Ronchi, E. & Fewtrell, L. 2003 *Assessing Microbial Safety of Drinking Water Improving Approaches and Methods*. World Health Organization (WHO) and Organization for Economic Co-operation and Development (ORCD), IWA Publishing Alliance House, London, UK.
- Duran, A. E., Muniesa, M., Moce-Llivina, L., Campos, C., Jofre, J. & Lucena, F. 2003 Usefulness of different groups of bacteriophages as model microorganisms for evaluating chlorination. *J. Appl. Microbiol.* **95**, 29–37.
- Edberg, S. C. & Smith, D. B. 1988 Absence of association between total heterotrophic and total coliform bacteria from a public water supply. *Appl. Environ. Microbiol.* **55**, 380–384.
- EIWID 2003 *Emerging Issues in Water and Infectious Diseases*. World Health Organization, Geneva, Switzerland.
- Fenwick, A. 2006 Waterborne Diseases: could they be consigned to history. *Science* **313**, 1077–1081.
- Field, K. G. & Samadpour, M. 2007 Fecal source tracking, the indicator paradigm, and managing water quality. *Water Res.* **41** (16), 3517–3538.
- Field, K. G., Bernhard, A. E. & Brodeur, T. J. 2003 Molecular approaches to microbiological monitoring: fecal source detection. *Environ. Monit. Assess.* **81**, 313–326.
- Figueras, M. J. & Borrego, J. J. 2010 New perspectives in monitoring drinking water microbial quality. *Int. J. Environ. Res. Public Health* **7**, 4179–4202.
- Figueras, M. J., Robertson, W., Pike, E. & Borrego, J. J. 2000 Sanitary inspection and microbiological water quality. In: *Monitoring Bathing Waters. A Practical Guide to the Design and Implementation of Assessments and Monitoring Programme* (J. Bartram & G. Rees, eds). E & FN Spon, London, UK pp. 113–167.
- Figueras, M. J., Collado, L. & Guarro, J. 2008 A new 16S rDNA-RFLP method for the discrimination of the accepted species of *Arcobacter*. *Microbiol. Infect. Dis.* **62**, 11–15.
- Fogarty, L. R. & Voytek, M. A. 2005 rRNA Genetic markers for fecal samples comparison of *Bacteroides-Prevotella* 16S from different animal species. *Appl. Environ. Microbiol.* **71** (10), 5999–6007.
- Fong, T. T. & Lipp, E. K. 2005 Enteric viruses of humans and animals in aquatic environments: health risks, detection, and potential water quality assessment tools. *Microbiol. Mol. Biol. Rev.* **69**, 357–371.
- Fong, T. T., Mansfield, L. S., Wilson, D. L., Schwab, D. J., Molloy, S. L. & Rose, J. B. 2007 Massive microbiological groundwater contamination associated with a waterborne outbreak in Lake Erie, South Bass Island, Ohio. *Environ. Health Prospect.* **115**, 856–864.
- Furtula, V., Osachoff, H., Derksen, G., Juahir, H., Colodey, A. & Chambers, P. 2012 Inorganic nitrogen, sterols and bacterial source tracking as tools to characterize water quality and possible contamination sources in surface water. *Water Res.* **46**, 1079–1092.
- Gawler, A. H., Beecher, J. E., Brandao, J., Carroll, N. M., Falcao, L., Gourmelon, M., Masterson, B., Nunes, B., Portera, J., Rinced, A., Rodrigues, R., Thorpf, M., Walters, J. M. & Meijer, W. G. 2007 Validation of host-specific Bacteroides 16S rRNA genes as markers to determine the origin of fecal pollution in Atlantic Rim countries of the European Union. *Water Res.* **41**, 3780–3784.
- Gerba, C. P. & Smith, J. E. 2005 Sources of pathogenic microorganisms and their fate during land application of wastes. *J. Environ. Qual.* **34**, 42–48.
- Giao, M. S., Azevedo, N. F., Wilks, S. A., Vieira, M. J. & Keevil, C. W. 2008 Persistence of *Helicobacter pylori* in heterotrophic drinking water biofilms. *Appl. Environ. Microbiol.* **74**, 5898–5904.
- Gilbride, K. A., Lee, D. Y. & Beaudette, L. A. 2006 Molecular techniques in wastewater: understanding microbial communities, detecting pathogens, and real-time process control. *J. Microbiol. Methods* **66**, 1–20.
- Girones, R., Ferrus, M. A., Alonso, J. L., Manzano, J. R., Calgua, B., Correa, A. D. A., Hundesa, A., Carratala, A. & Bofill-Mas, S. 2010 Molecular detection of pathogens in water – the pros and cons of molecular techniques. *Water Res.* **44**, 4325–4339.
- Gourmelon, M., Caprais, M. P., Ségura, R., Mennec, C. L., Lozach, S., Piriou, J. Y. & Rince, R. A. 2007 Evaluation of two-library-independent microbial source tracking methods to identify sources of fecal contamination in French estuaries. *Appl. Environ. Microbiol.* **3**, 4857–4866.
- Gunnarsdóttir, M. J. & Gissurarson, L. R. 2008 HACCP and water safety plans in icelandic water supply: preliminary evaluation of experience. *J. Water Health* **6**, 377–382.

- Harvey, R. W. 1997 Microorganisms as tracers in ground water injection and recovery experiments: a review. *FEMS Microbiol. Rev.* **20**, 461–472.
- Harwood, V. J., Brownell, M., Wang, S., Lepo, J., Ellender, R. D., Ajidahun, A., Hellein, K. N., Kennedy, E., Ye, X. & Flood, C. 2009 Validation and field testing of library-independent microbial source tracking methods in the Gulf of Mexico. *Water Res.* **43** (19), 4812–4819.
- Havelaar, A. H. & Pot-Hogbeem, W. H. 1988 F-specific RNA-bacteriophages as model viruses in water hygiene: Ecological aspects. *Water Sci. Technol.* **20**, 399–407.
- Hazen, T. C. & Toranzos, G. A. 1990 Tropical source water. In: *Drinking Water Microbiology* (G. A. McFeters, ed.). Springer-Verlag, New York, USA, pp. 32–54.
- Health Canada 2006 *Technical Documents for the Guidelines for Canadian Drinking Water Quality: Bacterial Waterborne Pathogens – Current and Emerging Organisms of Concern*. The authority of Minister of Health. Health Canada. Ottawa, Ontario. Available from <http://healthcanada.gc.ca>.
- Health Canada 2013 *Guidance on Providing Safe Drinking Water in Areas of Federal Jurisdiction*. Version 2. Minister of Health, Canada. Pub. Number: 130373.
- Horman, A., Rimhanen-Finne, R., Maunula, L., Bonsdorff, C. H., Torvela, N., Heikinheimo, A. & Hanninen, M. L. 2004 *Campylobacter* spp., *Giardia* spp., *Cryptosporidium* spp., Noroviruses, and indicator organisms in surface water in southwestern Finland. *Appl. Environ. Microbiol.* **70**, 87–95.
- Hot, D., Legeay, O., Jacques, J., Gantzer, C., Caudrelier, Y., Guyard, K., Lange, M. & Andreoletti, L. 2003 Detection of somatic phages, infectious enteroviruses and enterovirus genomes as indicators of human enteric viral pollution in surface waters. *Water Res.* **37**, 4703–4710.
- Hrudey, S. E. 2011 *Safe Drinking Water Policy for Canada – Turning Hindsight into Foresight. Commentary*. C. D. Howe Institute, Toronto, ON.
- Hundesda, A., Maluquer de Motes, C., Bofill-Mas, S., Albinana-Gimenez, N. & Girones, R. 2006 Identification of human and animal adenoviruses and polyomaviruses for determination of sources of fecal contamination in the environment. *Appl. Environ. Microbiol.* **72**, 7886–7893.
- Hurst, C. J., Crawford, R. L., Knudsen, G. R., McInerney, M. J. & Stetzenbach, L. D. 2002 *Manual of Environmental Microbiology*. ASM Press, Washington, DC.
- Isobe, K. O., Tarao, M., Zakaria, M. P., Chiem, N. H., Minh, L. Y. & Takada, H. 2002 Quantitative application of fecal sterols using gas chromatography–mass spectrometry to investigate fecal pollution in tropical waters: western Malaysia and Mekong Delta, Vietnam. *Environ. Sci. Technol.* **36**, 4497–4507.
- Isobe, K. O., Tarao, M., Chiem, N. H., Minh, L. Y. & Takada, H. 2004 Effect of environmental factors on the relationship between concentrations of coprostanol and fecal indicator bacteria in tropical (Mekong Delta) and temperate (Tokyo) freshwaters. *Appl. Environ. Microbiol.* **70**, 814–821.
- Kahlisch, L., Henne, K., Groebe, L., Draheim, J., Hofle, M. G. & Brettar, I. 2010 Molecular analysis of the bacterial drinking water community with respect to live/dead status. *Water Sci. Technol.* **61**, 9–14.
- Karanis, P., Kourenti, C. & Smith, H. 2007 Waterborne transmission of protozoan parasites: a worldwide review of outbreaks and lessons learnt. *J. Water Health.* **5**, 1–18.
- Keer, J. T. & Birch, L. 2003 Molecular methods for the assessment of bacterial viability. *J. Microbiol. Methods* **53**, 175–183.
- King, E. L., Bachoon, D. S. & Gates, K. W. 2007 Rapid detection of human fecal contamination in estuarine environments by PCR targeting of *Bifidobacterium adolescentis*. *J. Microbiol. Methods* **68**, 76–81.
- Koster, W., Egli, T., Ashbolt, N., Botzenhart, K., Burlion, N., Endo, T., Grimont, P., Guillot, E., Mabilat, C., Newport, L., Niemi, M., Payment, P., Prescott, A., Renaud, P. & Rust, A. 2003 *Assessing Microbial Safety of Drinking Water: Improving Approaches and Methods*. OECD, World Health Organization, Geneva, Switzerland, pp. 237–292.
- Kreder, C. A. 1995 Design and evaluation of Bacteroides DNA probes for the specific detection of human fecal pollution. *Appl. Environ. Microbiol.* **61**, 1171–1179.
- Lamendella, R., Santo Domingo, J. W., Kelty, C. & Oerther, D. B. 2008 Bifidobacteria in feces and environmental waters. *Appl. Environ. Microbiol.* **74** (3), 575–584.
- Layton, B. A., Walters, S. P., Lam, L. H. & Boehm, A. B. 2010 Enterococcus species distribution among human and animal hosts using multiplex PCR. *J. Appl. Microbiol.* **109**, 539–547.
- Leclerc, H., Edberg, S., Pierzo, V. & Delattre, J. M. 2000 Bacteriophages as indicators of enteric viruses and public health risk in ground waters. *J. Appl. Microbiol.* **88**, 5–21.
- Leclerc, H., Mossel, D. A. A., Edberg, S. C. & Struijk, C. B. 2001 Advances in the bacteriology of the coliform group: their suitability as markers of microbial water safety. *Annu. Rev. Microbiol.* **55** (1), 201–234.
- Lepeuple, A. S., Gaval, G., Jovic, M. & Roubin de, M. R. 2004 Literature review on levels of pathogens and their abatement in sludges, soil and treated biowaste. Horizontal project-6, WP3: Hygienic parameters. Available from: [www.ecn.nl/docs/society/horizontal/hor6-pathogens.pdf](http://www.ecn.nl/docs/society/horizontal/hor6-pathogens.pdf).
- Maal-Bared, R., Bartlett, K. H. & Bowie, W. R. 2008 Dealing with waterborne disease in Canada: challenges in the delivery of safe drinking water. *Rev. Environ. Health* **23** (2), 119–133.
- Marcelino, L. A., Backman, V., Donaldson, A., Steadman, C., Thompson, J. R., Preheim, S. P., Lien, C., Lim, E., Veneziano, D. & Polz, M. F. 2006 Accurately quantifying low-abundant targets amid similar sequences by revealing hidden correlations in oligonucleotide microarray data. *Proc. Natl Acad. Sci. USA* **103** (37), 13629–13634.
- Maynard, C., Berthiaume, F., Lemarchand, K., Harel, J., Payment, P., Bayardelle, P., Masson, L. & Brousseau, R. 2005 Waterborne pathogen detection by use of oligonucleotide-based microarrays. *Appl. Environ. Microbiol.* **71** (12), 8548–8557.
- McFeters, G. A. 1990 Enumeration, occurrence and significance of injured indicator bacteria in drinking water. In: *Drinking Water Microbiology*. Springer-Verlag, New York, USA, pp. 478–492.

- McFeters, G. A., Bissonnette, G. K., Jezeski, J. J., Thomson, C. A. & Stuart, D. G. 1974 Comparative survival of indicator bacteria and enteric pathogens in well water. *Appl. Environ. Microbiol.* **27**, 823–829.
- Meays, C. L., Broersm, K., Nordin, R. & Mazumder, A. 2004 Source tracking fecal bacteria in water: a critical review of current methods. *J. Environ. Manage.* **73**, 71–79.
- Mendez, J., Audicana, A., Cancer, M., Isern, A., Llaneza, J., Moreno, B., Navarro, M., Tarancon, M. L., Valero, F., Ribas, F., Jofre, J. & Lucena, F. 2004 Assessment of drinking water quality using indicator bacteria and Bacteriophages. *J. Water Health* **2** (3), 201–214.
- Metcalf & Eddy 1991 *Wastewater Engineering: Treatment and Reuse*. 1st edn, McGraw Hill, New York.
- Metcalf & Eddy 2003 *Wastewater and Engineering, Treatment and Reuse*. 4th edn, McGraw-Hill, New York.
- Miernik, A. 2004 Occurrence of bacteria and coli bacteriophages as potential indicators of fecal pollution of Vistula River and Zegrze Reservoir. *Polish J. Environ. Studies* **13**, 79–84.
- Morens, D. M. & Fauci, A. S. 2013 Emerging infectious diseases: threats to human health and global stability. *PLoS Pathog.* **9** (7), pe1003467.
- Muniesa, M., Lucena, F., Blanch, A. R., Payan, A. & Jofre, J. 2012 Use of abundance ratios of somatic coliphages and bacteriophages of *Bacteroides thetaiotaomicron* GA17 for microbial source identification. *Water Res.* **46**, 6410–6418.
- Mushi, D., Byamukama, D., Kivaisi, A. K., Mach, R. L. & Farnleitner, A. H. 2010 Sorbitol-fermenting Bifidobacteria are indicators of very recent human faecal pollution in streams and groundwater habitats in urban tropical lowlands. *J. Water Health* **8** (3), 466–478.
- National Research Council (NRC) 2004 *Indicators for Waterborne Pathogens and Evaluation of Risk: A Phased Approach to Monitoring Microbial Water Quality*. The National Academic Press, Washington, DC, USA, pp. 13–16.
- Noble, R. T., Allen, S. M., Blackwood, A. D., Chu, W., Jiang, S. C., Lovelace, G. L., Sobsey, M. D., Stewart, J. R. & Wait, D. A. 2003 Use of viral pathogens and indicators to differentiate between human and non-human fecal contamination in a microbial source tracking comparison study. *J. Water Health* **1**, 195–208.
- Nwachuku, N. & Gerba, C. P. 2004 Emerging waterborne pathogens: can we kill them all? *Curr. Opin. Biotechnol.* **15**, 175–180.
- O'Reilly, C. E., Bowen, A. B., Perez, N. E., Sarisky, J. P., Shepherd, C. A., Miller, M. D., Hubbard, B. C., Herring, M., Buchanan, S. D., Fitzgerald, C. C., Hill, V., Arrowood, M. J., Xiao, L. X., Hoekstra, R. M., Mintz, E. D. & Lynch, M. F. 2007 A waterborne outbreak of gastroenteritis with multiple etiologies among resort island visitors and residents. *Clin. Infect. Dis.* **44**, 506–512.
- Odonkor, S. T. & Ampofo, J. K. 2013 *Escherichia coli* as an indicator of bacteriological quality of water: an overview. *Microbiol. Res.* **4**, e2, 5–11.
- Okabe, S., Okayama, N., Savichtcheva, O. & Ito, T. 2006 Quantification of host-specific *Bacteroides-Prevotella* 16S rRNA genetic markers for assessment of fecal pollution in freshwater. *Appl. Microbiol. Biotechnol.* **74**, 894–901.
- Paul, J. H., Rose, J. B., Brown, J., Shinn, E. A., Miller, S. & Farrah, S. R. 1995 Viral tracer studies indicate contamination of marine waters by sewage disposal practices in Key Largo Florida. *Appl. Environ. Microbiol.* **61**, 2230–2234.
- Payment, P., Waite, M. & Dufour, A. 2003 Introducing parameters for the assessment of drinking water quality. In: *Assessing Microbial Safety of Drinking Water. Improving Approaches and Method*. WHO & OECD, IWA Publishing, London, UK, pp. 47–77.
- Petrini, B. 2006 *Mycobacterium abscessus*: an emerging rapid growing potential pathogen. *APMIS* **114**, 319–328.
- Pinto, V. G., Heller, L. & Bastos, R. K. X. 2012 Drinking water standards in South American countries: convergences and divergences. *J. Water Health* **10**, S295–S310.
- Pote, J., Haller, L., Kottelat, R., Sastre, V., Arpagaus, P. & Wildi, W. 2009 Persistence and growth of faecal culturable bacterial indicators in water column and sediments of Vidy Bay, Lake Geneva, Switzerland. *J. Environ. Sci.* **21**, 62–69.
- Raymaekers, M., Smets, R., Maes, B. & Cartuyvels, R. J. 2009 Checklist for optimization and validation of real-time PCR assays. *Clin. Lab. Anal.* **23** (3), 145–151.
- Rozen, Y. & Belkin, S. 2001 Survival of enteric bacteria in seawater. *FEMS Microbiol. Rev.* **25**, 513–529.
- Sauer, E. P., VandeWalle, J. L., Bootsma, M. J. & McLellan, S. L. 2011 Detection of the human specific *Bacteroides* genetic marker provides evidence of widespread sewage contamination of storm water in the urban environment. *Water Res.* **45**, 4081–4091.
- Savichtcheva, O. & Okabe, S. 2006 Alternative indicators of fecal pollution: relations with pathogens and conventional indicators, current methodologies for direct pathogen monitoring and future application perspectives. *Water Res.* **40**, 2463–2476.
- Scheutz, F. & Strockbine, N. A. 2005 Genus *Escherichia*. In: *Bergey's Manual of Systematic Bacteriology* (G. M. Garrity, ed.). 2nd edn, Springer, New York, USA, pp. 607–623.
- Scott, T. M., Rose, J. B., Jenkins, T. M., Farrah, S. R. & Lukasik, J. 2002 Microbial source tracking: current methodology and future directions. *Appl. Environ. Microbiol.* **68** (12), 5796–5803.
- Seas, C., Alarcon, M., Aragon, J. C., Beneit, S., Quinonez, M., Guerra, H. & Gotuzzo, E. 2009 Surveillance of bacterial pathogens associated with acute diarrhea in Lima, Peru. *Int. J. Infect. Dis.* **4**, 96–99.
- Seurinck, S., Defoirdt, T., Verstraete, W. & Siciliano, D. 2005 Detection and quantification of the human-specific HF183 *Bacteroides* 16S rRNA genetic marker with real-time PCR for assessment of human faecal pollution in freshwaters. *Environ. Microbiol.* **7**, 249–259.
- Seurinck, S., Verdriev, M., Verstraete, W. & Siciliano, S. D. 2006 Identification of human fecal pollution sources in a coastal area: a case study at Oostende (Belgium). *J. Water Health.* **4**, 167–175.

- Sharma, S., Sachdeva, P. & Viridi, J. S. 2003 Emerging water-borne pathogens. *Appl. Microbiol. Biotechnol.* **61**, 424–428.
- Sherchand, J. B. 2012 Future emerging issues in waterborne diseases and microbial agents. *J. Inst. Med.* **34** (3), 1–3.
- Simpson, J. M., Santo Domingo, J. W. & Reasoner, D. J. 2002 Microbial source tracking: state of the science. *Environ. Sci. Technol.* **36** (24), 5279–5288.
- Simpson, J. M., Santo Domingo, J. W. & Reasoner, D. J. 2004 Assessment of equine fecal contamination: the search for alternative bacterial source-tracking targets. *FEMS Microbiol. Ecol.* **47**, 65–75.
- Sinclair, R. G., Jones, E. L. & Gerba, C. P. 2009 Viruses in recreational water-borne disease outbreaks: a review. *J. Appl. Microbiol.* **107**, 1769–1780.
- Sinton, L. W., Finlay, R. K. & Hannah, D. J. 1998 Distinguishing human from faecal freshwater contamination in water: a review. *New Zealand J. Marine Res.* **32**, 323–348.
- Skovgaard, N. 2007 New trends in emerging pathogens. *Int. J. Food Microbiol.* **120**, 217–224.
- Solo-Gabriele, H. M., Wolfert, M. A., Desmarais, T. R. & Palmer, C. J. 2000 Sources of *E. coli* in a coastal subtropical environment. *App. Environ. Microbiol.* **66**, 230–237.
- Staradumskyte, D. & Paulauskas, A. 2012 Indicators of microbial drinking and recreational water quality. *Biologija* **58**, 7–13.
- Stewart, J. R., Gast, R. J., Fujioka, R. S., Solo-Gabriele, H. M., Meschke, J. S., Amaral-Zettler, L. A., Castillo, E., Polz, M. F., Collier, T. K., Strom, M. S., Sinigalliano, C. D., Moeller, P. D. R. & Holland, A. F. 2008 The coastal environment and human health: microbial indicators, pathogens, sentinels and reservoirs. *Environ. Health* **7** (Suppl. 2), pS3.
- Straub, T. M., Pepper, I. L. & Gerba, C. P. 1993 Hazards from pathogenic microorganisms in land-disposed sewage sludge. *Rev. Environ. Contam. Toxicol.* **132**, 55–91.
- Straub, T. M., Dockendorff, B. P., Quinonez-Diaz, M. D., Valdez, C. O., Shutthanandan, J. I., Tarasevich, B. J., Grate, J. W. & Bruckner-Lea, C. J. 2005 Automated methods for multiplexed pathogen detection. *J. Microbiol. Methods* **62** (3), 303–316.
- Tallon, P., Magajna, B., Lofranco, C. & Leung, K. T. 2005 Microbial indicators of faecal contamination in water: a current perspective. *Water Air Soil Pollut.* **166**, 159–166.
- Toranzos, G. A., McFeters, G. A., Borrego, J. J. & Savill, M. 2007 Detection of microorganisms in environmental freshwaters and drinking waters. In: *Manual of Environmental Microbiology*, 3rd edn, American Society for Microbiology Press, Washington, DC, USA, pp. 249–264.
- Toze, S. 2006 Water reuse and health risks – real vs. perceived. *Desalination* **187**, 41–51.
- Tree, J. A., Adams, M. R. & Lees, D. N. 2003 Chlorination of indicator bacteria and viruses in primary sewage effluent. *Appl. Environ. Microbiol.* **69**, 2038–2043.
- Tyagi, V. K., Chopra, A. K., Kazmi, A. A. & Kumar, A. 2006 Alternative microbial indicators of faecal pollution: current perspective. *Iran. J. Environ. Health Sci. Eng.* **3** (3), 205–216.
- Verhille, S. 2013 Understanding microbial indicators for drinking water assessment: interpretation of test results and public health significance. National collaborating centre for environmental health. 1–12. Available from: [www.nceh.ca/sites/default/files/Microbial\\_Indicators\\_Jan\\_electroniclink\\_2013\\_0.pdf](http://www.nceh.ca/sites/default/files/Microbial_Indicators_Jan_electroniclink_2013_0.pdf).
- Viau, E. J. & Boehm, A. B. 2011 Quantitative PCR-based detection of pathogenic *Leptospira* in Hawaiian coastal streams. *J. Water Health* **9** (4), 637–646.
- Vierheilig, J., Frick, C., Mayer, R. E., Kirschner, A. K. T., Reischer, G. H., Derx, J., Mach, R. L., Sommer, R. & Farnleitner, A. H. 2013 *Clostridium perfringens* is not suitable for the indication of fecal pollution from ruminant wildlife but is associated with excreta from nonherbivorous animals and human sewage. *Appl. Environ. Microbiol.* **79** (16), 5089–5092.
- Wade, T. J., Pai, N., Eisenberg, J. N. S. & Colford, J. M. 2003 U.S. Environmental Protection Agency water quality guidelines for recreational waters prevent gastrointestinal illness? A systematic review and meta-analysis. *Environ. Health Perspect.* **111** (8), 1102–1109.
- Ward, D. M., Weller, R. & Bateson, M. M. 1990 16S rRNA sequences reveal numerous uncultured microorganisms in a natural community. *Nature* **345**, 63–65.
- Wery, N., Lhoutellier, C., Ducray, F., Delgenes, J. P. & Godon, J. J. 2008 Behaviour of pathogenic and indicator bacteria during urban wastewater treatment and sludge composting, as revealed by quantitative PCR. *Water Res.* **42**, 53–62.
- Wery, N., Monteil, C., Pourcher, A. M. & Godon, J. J. 2010 Human-specific fecal bacteria in wastewater treatment plant effluents. *Water Res.* **44** (6), 1873–1883.
- Whiley, H., Keegan, A., Giglio, S. & Bentham, R. 2012 *Mycobacterium avium* complex – the role of potable water in disease transmission. *J. Appl. Microbiol.* **113**, 223–232.
- Wilson, M. 2005 *Microbial Inhabitants of Humans, their Ecology and Role in Health and Disease*. Cambridge University Press, Cambridge, UK.
- World Health Organization 2004 The microbiology of piped distribution systems and public health. In: *Safe Piped Water: Managing Microbial Water Quality in Piped Distribution System* (R. Ainsworth, ed.). IWA Publishing, London, UK.
- World Health Organization 2007 *Combating Waterborne Disease at the Household Level/International Network to Promote Household Water Treatment and Safe Storage*. World Health Organization, Geneva, Switzerland, pp. 1–36.
- World Health Organization 2008 *Guidelines for Drinking Water Quality*. 3rd edn, Geneva, Switzerland.
- Yates, M. V. 1998 *Pathogens in Reclaimed Wastewater*. University of California, California.
- Zheng, Y., Kelly, W. R., Panno, S. V. & Liu, W. T. 2013 *Identification of Sources of Fecal Pollution of Karst Waters*. Contract Report 2013-02. Available from: [www.isws.illinois.edu/pubdoc/CR/ISWSCR2013-02.pdf](http://www.isws.illinois.edu/pubdoc/CR/ISWSCR2013-02.pdf).